

POSTER PRESENTATION

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Human cytomegalovirus glycoprotein N polymorphisms among renal transplant recipients in India

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Background

Human Cytomegalovirus (HCMV) is one of the most common infectious complications in renal transplant recipients. Extensive genetic polymorphisms in envelope glycoproteins of HCMV have been demonstrated among clinical HCMV isolates. Some previous studies have proposed the potential linkage between HCMV gN genotype to the frequency of symptomatic infection and clinical outcome in renal transplant recipients. No data available on circulating HCMV strains among renal transplant recipients in India.

Objective

To determine the cytomegalovirus strain diversity in renal transplant recipients.

Methods

One hundred thirty two renal transplant recipients were included in this study. DNA extracted from blood samples by Qiagen kit method. Specimen DNA was amplified by PCR using glycoprotein N (gN) gene primers. Genotyping was carried out by RFLP and results were confirmed by direct and/or cloning followed by nucleotide sequencing of the plasmid DNA of selected strains.

Results

HCMV detected by PCR for gN gene in the 83(63%) samples and sixty seven of these samples were typed by RFLP. Among these gN1 was identified in 17(25.3 %) cases. None of the samples contained gN2 genotype,

gN3 genotype detected in 9(13.4%) cases, while gN4 strain was identified in 23 cases (34.3%), respectively. Infection with multiple gN type was seen in 18(27 %) of the samples.

Conclusion

The results of our study showed that gN4 was the commonest gN genotype found followed by gN1. This study was supported by the Indian Council of Medical Research, Government of India.

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